

-43 ATACTGGCTCAACCTCGGAGCTCACACTCAGGCTGGCGGGCC

-26 Met Gly Arg Arg Val Pro Ala Leu Arg Gln Leu Val Leu Leu Leu Leu Leu Leu Leu Leu Leu Leu Gln
 1 ATG GGG CGG CGA GTC CCA GCT CTG AGA CAG CAG CTG CTG CTG CTG CTG CTG CTG CTG CTG CTG CTG CTG CAG CTG CAG CTG CAG
 -1 Ser Arg Glu Glu Leu Ser Gly Ser Arg Cys Pro Glu Pro Glu Cys Asp Cys Ala Pro Asp Gly Ala Leu Arg Cys Pro Gly
 76 TCC CGA GAG CTG TCA GGG TCG TCG GGC CCC GAG CCC GAG CCC TGC GAC TGC GCA CCG GAT GGC GCC CTG CGC TGT CCT GGC
 25 Pro Arg Ala Gly Leu Ala Arg Leu Ser Leu Thr Thr Tyr Leu Pro Val Lys Val Ile Pro Ser Gln Ala Phe Arg Gly
 151 CCT CGA GCC GGC CTC GTC GAA ATT GAA ATC TCT TCT ACC CTC ACC TAT TAT CTC CCT CCT GTC AAA GTA ATT CCA TCA CAA GCT TTC AGG GGA
 50 Leu Asn Glu Val Lys Ile Glu Ile Ser Gln Ser Asp Ser Leu Glu Arg Ile Glu Ala Asn Ala Phe Asp Asn
 226 CTT AAT GAG GTC GTA AAA ATT GAA ATC TCT CAG AGT GAT TCC CTG GAA AGG ATA GAA GCT AAT GCC TTT GAC AAC
 75 Leu Leu Asn ▼ Leu Ser Glu Leu Leu Ile Gln Asn Thr Lys Asn Leu Tyr Ile Glu Pro Gly Ala Phe Thr Asn
 301 CTC CTC AAT TTG TCT GAA CTA CTG ATC CAG AAC ACC AAA Lys Leu Leu Tyr Ile Glu Pro Gly Ala Phe Thr Asn
 100 Leu Pro Arg Leu Lys Tyr Leu Ser Ile Cys Asn Thr Gly Ile Arg Thr Leu pro Asp Val Thr Lys Ile Ser Ser
 376 CTC CCT CGG TTA AAA TAC CTG AGC ATC TGT AAC ACA GGC ATC CGA ACC CTT CCA GAT GTT ACG AAG ATC ATC TCC TCC
 125 Ser Glu Phe Asn Phe Ile Leu Glu Ile Cys Asp Asn Leu His Ile Thr Thr Thr Ile Pro Gly Asn Ala Phe Gln Gly
 451 TCT GAA TTT AAT TTC ATT CTG GAA ATC TGT GAT AAC TTA CAC ATA ACC ACC ATA CCC GGG AAT GCT TTC CAA GGG
 150 Met Asn Asn ▼ Glu Ser Val Thr Leu Lys Leu Tyr Glu Asn Gly Phe Glu Glu Val Gln Ser His Ala Phe Asn Gly
 526 ATG AAT AAC GAG TCT GTC ACA CTA AAA CTA AAA CTA TAT GGA AAT GGA TTT GAA GAA GTA CAA AGC CAT GCA TTC AAT GGG
 175 Thr Thr Leu Ile Ser Leu Glu Leu Lys Glu Asn Ile Tyr Leu Glu Lys Met His Ser Gly Ala Phe Gln Gly Ala
 601 ACG ACT CTA ATC TCG CTG GAG CTA AAA GAA AAC ATC TAC CTG GAG AAG ATG CAC AGT GGA GCC TTC CAG GGG GCC
 200 Thr Gly Pro Ser Ile Leu Asp Ile Ser Ser Thr Ser Thr Lys Leu Gln Ala Leu Pro Ser His Gly Leu Glu Ser Ile Gln
 676 ACG GGG CCC AGC ATC CTG GAT ATT TCT TCT ACC AAA TTTG CAG GCC CTG CCG AGC CAC GCG CAC GGG CTG GAG TCC ATT CAG
 225 Thr Leu Ile Ala Leu Ser Ser Tyr Ser Leu Lys Thr Leu Pro Ser Lys Glu Lys Phe Thr Ser Leu Leu Val Ala
 751 ACG CTC ATC GCC CTG TCT TCC TAC TCA CTG AAA ACA CTG CCC TCC AAA GAA AAA TTC ACG AGC CTC CTG GTC GCC
 250 Thr Leu Thr ▼ Tyr Pro Ser His Cys Cys Ala Phe Arg Asn Leu Pro Lys Lys Glu Asn Phe Ser Phe Ser Ile
 826 ACG CTG ACC TAC CCC AGC CAC TGC TGC TGC GCC TTC AGG AAT TTG CCG AAG AAA GAA GAA CAG AAT TTT TCA TTT TCC ATT
 275 Phe Glu Asn Phe Ser Lys Gln Cys Glu Cys Glu Ser Thr Val Arg Lys Ala Asp Asn Glu Thr Thr Ser Ala Ile Phe
 901 TTT GAA AAC TTC TCC AAA CAA CAA GTT AGA AAA GCA GAT AAC GAG ACN Thr Thr Ser Ala Ile Phe

Fig. 1B.

300 Glu Glu Asn Glu Leu Ser Gly Trp Asp Tyr Gly Phe Cys Ser Pro Lys Thr Leu Gln Cys Ala Pro Glu
 976 GAG GAG AAT GAA CTC AGT AGT GGC TGG GAT TAT GAT TAT GGC TTC TCA CCC AAG ACA CTC CAA TGT GCT CCA GAA

325 Pro Asp Ala Phe Asn Pro Cys Glu Asp Ile Met Gly Tyr Ala Phe Leu Arg Val Leu Ile Trp Leu Ile Asn Ile
 1051 CCA GAT GCT TTC AAC CCC TGT GAA GAT ATT ATG GGC TAT GCC TTC CTT AGG GTC CTG ATT TGG CTG ATT AAT ATA

350 Leu Ala Ile Phe Gly Asn Leu Thr Val Phe Leu Leu Thr Ser Arg Tyr Lys Leu Thr Val Pro Arg Phe
 1126 CTA GCC ATC TTT GGC AAC CTG ACA GTC CTC TTT GTT CTC CTC ACC AGT CGT TAT AAA CTG ACA GTG CCC CGC TTC

375 Leu Met Cys Asn Leu Ser Phe Ala Asp Phe Cys Met Gly Leu Tyr Leu Leu Ile Ala Ser Val Asp Ser Gln
 1201 CTC ATG TGT AAT CTC TCC TTT GCA GAC TTT TGC ATG GGG CTC TAC CTG CTG CTC ATT GCC TCC GTG GAC TCC CAA

400 Thr Lys Gly Gln Tyr Tyr Asn His Ala Ile Asp Trp Gln Thr Gly Ser Gly Cys Gly Ala Ala Gly Phe Phe Thr
 1276 ACA AAA GGC CAG TAC TAT AAC CAC GCC ATA GAC TGG CAG ACA GGG AGT GGC TGC GGT GCA GCT GGC TTC TTT ACT

425 Val Phe Ala Ser Glu Leu Ser Val Tyr Thr Leu Thr Val Ile Thr Leu Glu Arg Trp His Thr Ile Thr Tyr Ala
 1351 GTG TTT GCC AGT GAA CTC TCT GTC TAC ACC CTG ACG GTT ATC ACC CTG GAA AGG TGG CAC ACC ATC ACC TAT GCT

450 Val Gln Leu Asp Gln Lys Leu Arg CTA AGA CTG AGG CAT Ala Ile Pro Ile Met Leu Gly Gly Trp Leu Phe Ser Thr Leu
 1426 GTA CAG CTA GAC CAA AAG CTA AGA CTG AGG CAT GCC ATC CCA ATT ATG CTC GGA TGG CTC TTT TCT ACG CTG

475 Ile Ala Thr Met Pro Leu Val Gly Ile Ser Asn Tyr Met Lys Val Ser Ile Cys Leu Pro Met Asp Val Glu Ser
 1501 ATC GCC ACG ATG CCC CTT GTG GGT ATC AGC AAT TAC ATG AAG GTC AGC ATC TGC CTC CCC ATG GAT GTG GAA TCC

500 Thr Leu Ser Gln Val Tyr Ile Leu Ser Ile Leu Asn Val Val Ala Phe Val Val Ile Cys Ala Cys Tyr
 1576 ACT CTG TCC CAA GTC TAC ATA TTA TCC ATC CTC AAC GTG GTG GCC TTC GTC GTC ATC TGT GCT TGC TAC

525 Ile Arg Ile Tyr Phe Ala Val Gln Asn Pro Glu Leu Thr Ala Pro Asn Lys Asp Thr Lys Ile Ala Lys Lys Met
 1651 ATT AGG ATC TAC TTT GCA GTT CAA AAT CCA GAG CTG ACA GCT CCT AAC AAG GAC ACA AAA ATT GCT AAG AAG ATG

Fig. 2A.

LH/CGR RHO SKR β-2AR 5HT-2R	TM-1																				
	339	F	L	R	V	L	I	W	L	I	N	I	L	A	I	F	G	N	L	T	V
	36	Q	F	S	M	L	A	A	Y	M	F	L	L	I	M	L	G	F	P	I	N
	35	L	W	T	A	A	Y	L	A	L	V	L	V	A	V	M	G	N	A	T	V
	35	G	M	G	I	V	M	S	L	I	V	L	A	I	V	F	G	N	V	L	V
53	W	S	A	L	L	T	T	V	V	I	I	L	T	I	A	G	N	I	L	V	I
LH/CGR RHO SKR β-2AR 5HT-2R	TM-2																				
	384																				
	84																				
	80																				
	80																				
99																					
LH/CGR RHO SKR β-2AR 5HT-2R	TM-3																				
	433																				
	126																				
	122																				
	122																				
142																					
LH/CGR RHO SKR β-2AR 5HT-2R	TM-4																				
	483																				
	175																				
	169																				
	172																				
191																					

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Fig. 2B.

TM-5

LH/CGR	S	N	Y	-	-	-	-	M	K	V	S	I	C	L	P	M	D	V	E	S	T	L	-	-	-	S	Q	V	Y	I	L	S	I	L	I	L	N	V	V	A	F	-	V	V	I	C	A	C	Y	I	R	526
RHO	S	R	Y	I	P	E	G	M	Q	C	S	C	G	I	D	Y	Y	T	P	H	E	E	T	N	N	E	S	F	V	I	Y	M	F	V	V	H	E	I	I	P	L	I	V	I	F	F	C	Y	G	Q	225	
SKR	S	T	I	T	T	D	E	G	A	T	K	C	V	V	A	W	P	E	D	S	G	G	K	M	L	L	Y	H	L	I	V	I	A	I	Y	F	L	P	L	V	V	M	F	V	A	Y	S	V	219			
B-2AR	W	Y	R	A	T	H	Q	E	A	I	N	C	Y	A	N	E	T	C	C	D	F	-	F	T	N	Q	A	Y	A	I	A	S	S	I	V	S	F	Y	V	P	L	V	I	M	V	F	V	Y	S	R	221	
5HT-2R	G	L	Q	D	D	S	K	V	F	K	E	G	S	C	L	L	A	D	-	-	-	-	-	-	-	-	-	D	N	F	V	L	I	G	S	F	V	A	F	I	P	L	T	I	M	V	I	T	Y	F	L	234

TM-6

LH/CGR	I	Y	F	A	V	Q	N	P	E	L	T	A	P	N	K	D	T	K	I	A	K	K	M	A	I	L	I	F	T	D	F	T	-	C	M	A	P	I	S	F	F	A	I	S	A	A	F	K	V	P	575
RHO	L	V	F	T	V	K	E	A	A	A	(8)	Q	K	A	E	K	E	V	T	R	M	V	I	I	M	V	I	A	F	L	I	C	W	L	P	Y	A	G	V	A	F	Y	I	F	T	H	Q	G	280		
SKR	I	Q	L	T	L	W	R	R	S	V	(12)	L	Q	A	K	K	F	V	K	T	M	V	L	V	V	V	T	F	A	I	C	W	L	P	Y	H	L	Y	F	I	L	G	T	F	Q	E	D	278			
B-2AR	V	F	Q	E	A	K	R	Q	L	Q	(33)	C	L	K	E	H	K	A	L	K	T	L	G	I	I	M	G	T	F	T	L	C	W	L	P	F	F	I	V	N	I	V	H	V	I	Q	D	N	301		
5HT-2R	T	I	K	S	L	Q	K	E	A	T	(48)	I	S	N	E	Q	K	A	C	K	V	L	G	I	V	F	F	L	F	V	V	M	C	P	F	F	I	T	N	I	M	A	V	I	C	K	E	329			

TM-7

LH/CGR	L	I	T	V	T	N	S	-	-	-	K	I	L	L	V	L	F	Y	P	V	N	S	C	A	N	P	F	L	Y	A	I	F	T	K	A	F	Q	R	D	F	L	L	L	L	S	R	F	G	C	621/674
RHO	S	D	F	G	P	I	F	-	-	-	M	T	I	P	A	F	F	A	K	T	S	A	V	Y	N	P	V	I	Y	I	M	N	K	Q	F	R	N	C	M	V	T	T	L	C	G	K	N	326/348		
SKR	I	Y	C	H	K	F	I	Q	Q	-	Y	L	A	L	F	W	L	A	M	S	S	T	M	Y	N	P	I	I	Y	C	C	L	N	H	R	F	R	S	G	F	R	L	A	F	C	P	W	327/384		
B-2AR	L	I	R	K	E	V	-	-	-	-	Y	I	L	L	N	W	I	G	Y	V	N	S	G	F	N	P	L	I	Y	-	C	R	S	P	D	F	R	I	A	F	Q	E	L	L	C	L	R	R	S	345/413
5HT-2R	S	C	N	E	N	V	I	G	A	L	L	N	V	F	V	W	I	G	Y	L	S	S	A	V	N	P	L	V	Y	T	L	F	N	K	T	Y	R	S	A	F	S	R	Y	I	Q	C	Q	Y	K	378/449

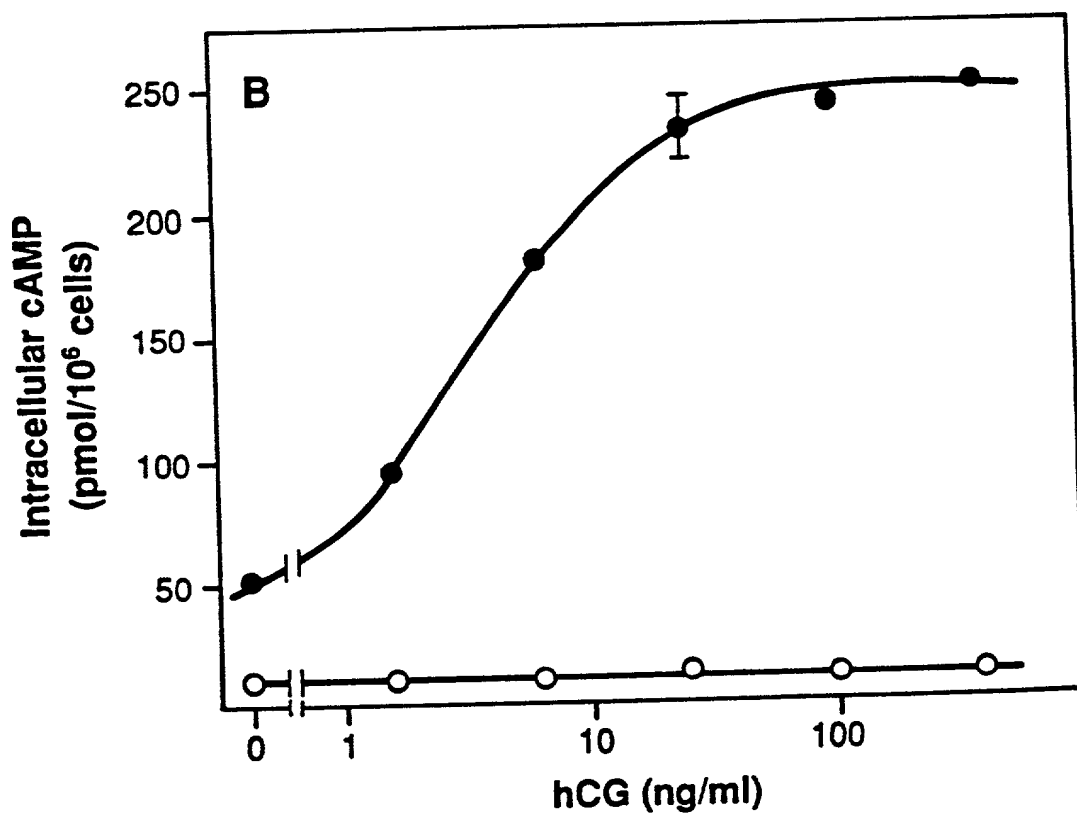
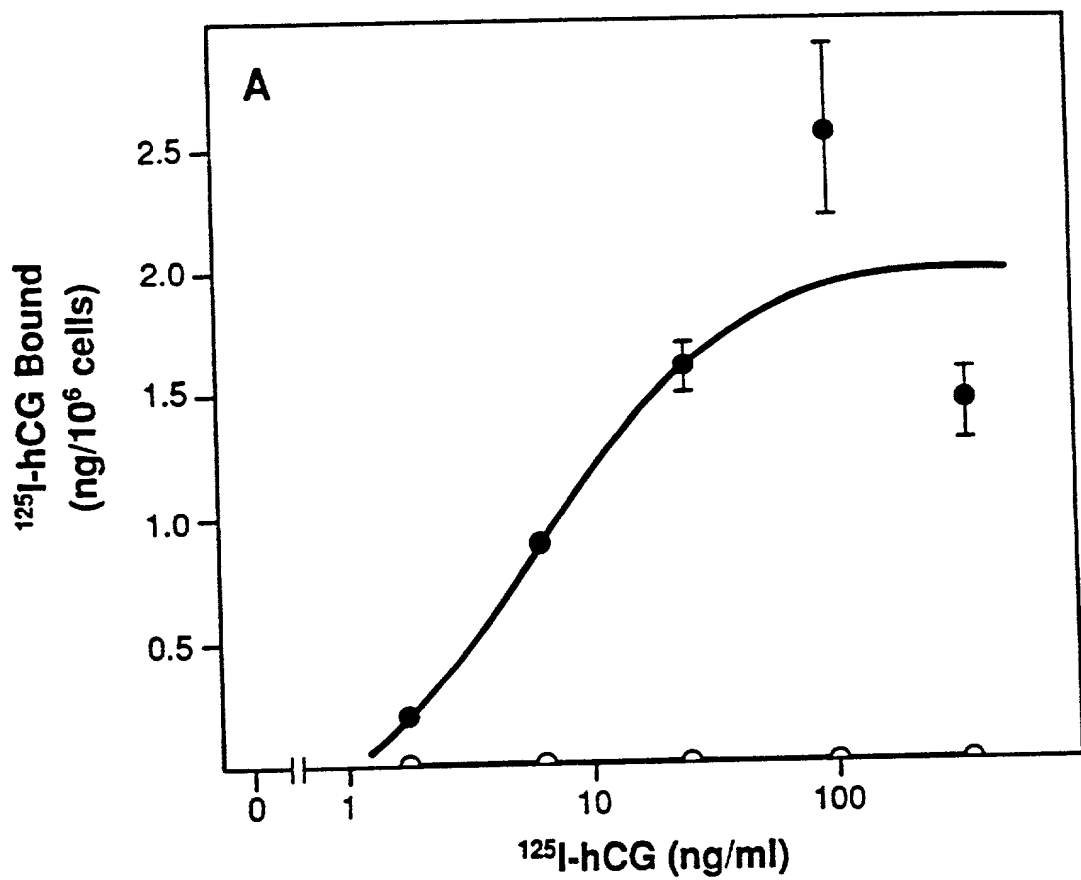
Fig. 3.

A		(1-11)	(12-38)	(39-63)	(64-88)	(89-112)	(113-138)	(139-164)	(165-187)	(188-211)	(212-233)	(234-251)	(252-273)	(274-290)	(291-318)	(319-341)
I	REL	SGS	RCPEP													
II	CDC	APD	G-													
III	VKV	IPSP	Q-													
IV	LERI	EAN-														
V	LYI	EPG-														
VI	RTL	PDV-														
VII	TTI	PGN-														
VIII	FEE	VQS	H-													
IX	LEK	MHS	G-													
X	LQA	LPS	H-													
XI	LKT	LPS	K-													
XII	-	-	-													
XIII	NET	LYS	A-													
XIV	LQC	AP	EP-													

B	LRG	Toll	GPIB	ACY
	LxxLPxx	xx	xx	xx
	LxxLPxx	xx	xx	xx
	LxxLPxx	xx	xx	xx
	axxaxxx	xx	xx	xx

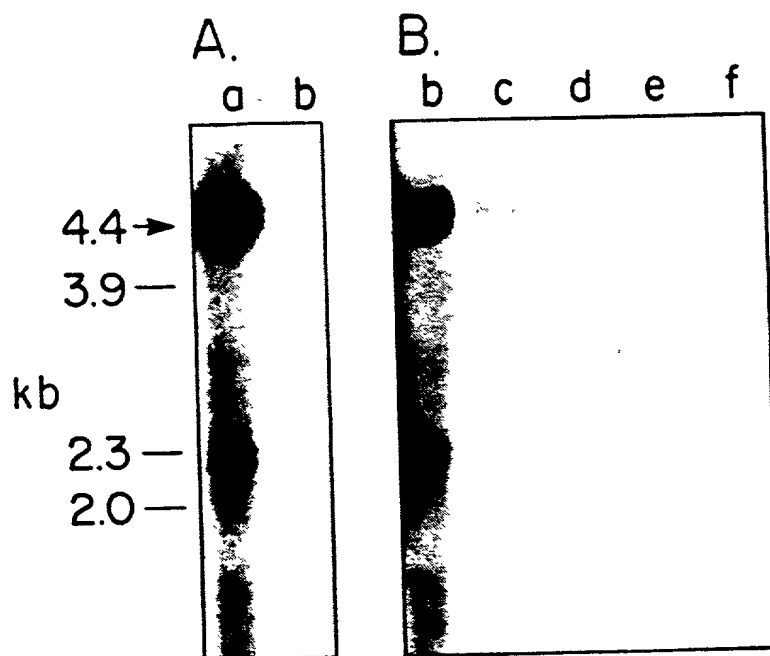
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Fig. 4.



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Fig. 5.



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Fig. 6A.

-71	AGGAGCCTGG	GGAATCTGTG	GAAGTTTTCG	CGCTGATGCA	GAAGAAAGT	CGGTGATGG
-10	ATAAATAAGG	ATG GCC TTG CTC CTG GTC TCC TTG CTG GCA TTC TTG GGC ACG GGA TCT GGA				
-17		Met Ala Leu Leu Cys His Cys Ser Asn Arg Val Phe Leu Ala Phe Leu Gly Thr Gly Ser Gly				
51	TGT CAT CAC	TGG CTG TGT CAT TGC TCT AAT AGG GTC TTT CTC TGC CAA GAC AGC AAG GTG				
1	Cys His	Thr Trip Leu Cys His Cys Ser Asn Arg Val Phe Leu Cys Gln Asp Ser Lys Val				
111	ACA GAG ATT	CCG ACC GAC CTC CCC CGG AAC GCC ATT GAA CTG AGG TTT GTG CTC ACC AAG				
21	Thr Glu Ile	Pro Thr Asp Leu Pro Arg Asn Ala Ile Glu Leu Arg Phe Val Leu Thr Lys				
171	CTT CGA GTC	ATC CCG AAA GGA TCA TTT GCT GGA TTT GGA GAC CTG GAG AAA ATA GAG ATC				
41	Leu Arg Val	Ile Pro Lys Gly Ser Phe Ala Gly Phe Gly Asp Leu Lys Ile Glu Ile				
231	TCT CAG AAT	GAT GTC TTG GAA GTA ATA GAG GCA GAT GTG TTC AAC CTA CCC AAG TTG				
61	Ser Gln Asn	Asp Val Leu Glu Val Ile Glu Ala Asp Val Phe Ser Asn Leu Pro Lys Leu				
291	CAT GAA ATT	AGG ATT GAA AAG GCC AAC AAT CTT CTG TAC ATC AAC CCG GAG GCC TTC CAG				
81	His Glu Ile	Arg Ile Glu Lys Ala Asn Asn Leu Leu Tyr Ile Asn Pro Glu Ala Phe Gln				
351	AAT CTC CCC	AGT CTC AGA TAT CTG TTA ATA TCC AAC ACA GGC ATT AAG CAC TTG CCA GCT				
101	Asn Leu Pro	Ser Ser Leu Arg Tyr Leu Leu Ile Ser Asn Thr Gly Ile Lys His Leu Pro Ala				
411	GTT CAC AAG	ATC CAG TCT CTC CAA AAG GTT CTA CTA GAC ATT CAA GAT AAC ATA AAC ATC				
121	Val His Lys	Ile Gln Ser Leu Gln Lys Val Leu Leu Asp Ile Gln Asp Asn Ile Asn Ile				
471	CAC ATC GTT	GCC AGG AAC TCC TTC ATG GGA CTG AGT TTT GAA AGT GTG ATT TTA TGG CTG				
141	His Ile Val	Ala Arg Asn Ser Phe Met Gly Leu Ser Phe Glu Ser Val Ile Leu Trip Leu				
531	AGT AAG AAT	GGG ATT GAA GAA ATA CAC AAC TGT GCA TTC AAC GGA ACT CAG CTA GAT GAA				
161	Ser Lys Asn	Gly Ile Glu Glu Ile His Asn Cys Ala Phe Asn Gly Thr Gln Leu Asp Glu				
591	CTG AAT CTA	AGC GAT AAC AAT AAT TTG GAA GAA TTG CCT AAT GAC GTT Phe Gln Gly Ala				
181	Leu Asn	Leu Ser Asp Asn Asn Asn Leu Glu Glu Leu Pro Asn Asp Val TTC CAG GGA GCC				
651	TCT GGG CCA	GTC ATT TTA GAT ATC TCA AGG ACA AAG GTC CAT TCC TTA CCA AAC CAT GGC				
201	Ser Gly Pro	Val Ile Leu Asp Ile Ser Arg Thr Lys Val His Ser Leu Pro Asn His Gly				
711	TTA GAA AAT	CTG AAG AAG CTG AGG GCC AGG TCA ACA TAC CGC TTG AAA AAG CTC CCT AAT				
221	Leu Glu Asn	Asn Leu Lys Lys Leu Arg Ala Arg Ser Thr Tyr Arg Leu Lys Lys Leu Pro Asn				
771	CTG GAC AAG	TTT GTC ACC CTC ATG GAG GCC AGC CTC ACC TAC CCC AGC CAC TGC TGT GCT				
241	Leu Asp Lys	Phe Val Thr Leu Met Glu Ala Ser Leu Thr Tyr Pro Ser His Cys Cys Ala				
831	TTT GCA AAC	TTG AAG CGG CAA ATC TCT GAA CTT CAT CCA ATT TGC AAC AAG TCT ATT TTA				
261	Phe Ala Asn	Asn Leu Lys Arg Gln Ile Ser Glu Leu His Pro Ile Cys Asn Lys Ser Ile Leu				
891	AGG CAA GAT	ATT GAT GAT ATG ACT CAA ATT GGG GAT CAG AGA GTC TCT CTG ATA GAT GAT				
281	Arg Gln Asp	Ile Asp Asp Met Thr Gln Ile Gly Asp Gln Arg Val Ser Leu Ile Asp Asp				
951	GAA CCC AGT	TAT GGA AAA GGA TCT GAC ATG ATG TAC AAT GAA TTT GAT TAT GAC TTA TGT				
301	Glu Pro Ser	Tyr Gly Lys Gly Ser Asp Met Tyr Asn Glu Phe Asp Tyr Asp Leu Cys				
1011	AAT GAA GTT	GTT GAT GTG ACC TGC TCA CCA AAG CCA GAT GCA TTT AAT CCA TGT GAA GAT				
321	Asn Glu Val	Val Asp Thr Cys Ser Pro Lys Pro Asp Ala Phe Asn Pro Cys Glu Asp				

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Fig. 6B.

I

II

III

IV

V

VI

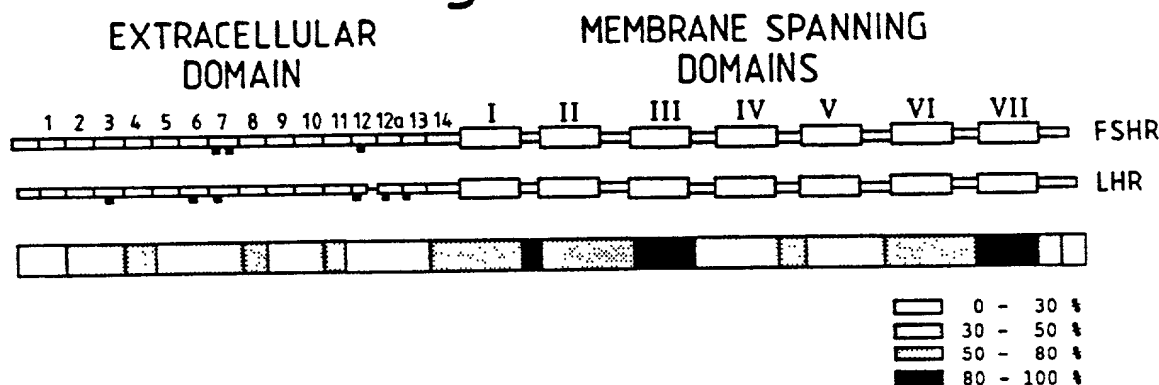
VII

1071	ATC	ATG	GGG	TAC	AAC	ATC	CTC	AGG	GTC	TTG	ATA	TGG	TTT	ATT	AGC	ATC	CTG	GCC	ATT	ACT
341	Ile	Met	Gly	Tyr	Asn	Ile	Leu	Arg	Val	Leu	Ile	Trp	Phe	Ile	Ser	Ile	Leu	Ala	Ile	Thr
1131	GGG	AAC	ACC	ACA	GTG	CTG	GTG	GTC	CTG	ACC	ACA	AGC	CAA	TAC	AAA	CTA	ACT	GTG	CCC	CGG
361	Gly	Asn	Thr	Thr	Val	Leu	Val	Val	Leu	Thr	Thr	Ser	Gln	Tyr	Lys	Leu	Thr	Val	Pro	Arg
1191	TTT	CTT	ATG	TGT	AAC	CTC	GCC	TTC	GCT	GAT	CTC	TGC	ATA	GGC	ATC	TAC	TTG	CTA	CTT	ATA
381	Phe	Leu	Met	Cys	Asn	Leu	Ala	Phe	Ala	Asp	Leu	Cys	Ile	Gly	Ile	Tyr	Leu	Leu	Ile	Ile
1251	GCA	TCA	GTT	GAC	ATC	CAT	ACC	AAG	AGC	CAG	TAC	CAC	AAC	TAT	GCC	ATT	GAC	TGG	CAA	ACA
401	Ala	Ser	Val	Asp	Ile	His	Thr	Lys	Ser	Gln	Tyr	His	Asn	Tyr	Ala	Ile	Asp	Trp	Gln	Thr
1311	GGA	GCA	GGC	TGT	GAT	GCT	GCT	GGC	TTT	TTC	ACT	GTC	TTT	GCC	AGT	GAA	CTG	TCA	GTC	TAC
421	Gly	Ala	Gly	Cys	Asp	Ala	Ala	Gly	Phe	Phe	Thr	Val	Phe	Ala	Ser	Glu	Leu	Ser	Val	Tyr
1371	ACA	TTG	ACA	GCC	ATC	ACC	CTA	GAA	AGA	TGG	CAT	ACC	ATC	ACA	CAT	GCT	ATG	CAA	CTG	GAA
441	Thr	Leu	Thr	Ala	Ile	Thr	Leu	Glu	Arg	Trp	His	Thr	Ile	Thr	His	Ala	Met	Gln	Leu	Glu
1431	TGC	AAG	GTG	CAG	CTC	CGG	CAT	His	Ala	Ser	Val	Met	Val	Leu	Gly	Trp	Thr	Phe	Ala	Phe
461	Cys	Lys	Val	Gln	Leu	Leu	Arg	His	Ala	Ala	Ser	Val	Met	Val	Leu	Gly	Trp	Thr	Phe	Ala
1491	GCA	GCT	GCT	CTC	TTC	CCC	ATC	TTT	GGC	ATC	AGT	AGC	TAC	ATG	AAA	GTG	AGC	ATC	TGC	CTG
481	Ala	Ala	Ala	Leu	Phe	Pro	Ile	Phe	Gly	Ile	Ser	Ser	Tyr	Met	Lys	Val	Ser	Ile	Cys	Leu
1551	CCC	ATG	GAT	ATC	GAC	AGC	CCT	TTG	TCA	CAG	CTG	TAT	GTT	ATG	GCC	CTC	CTT	GTC	CTC	AAT
501	Pro	Met	Asp	Ile	Asp	Ser	Pro	Leu	Ser	Gln	Leu	Tyr	Val	Met	Ala	Leu	Val	Leu	Asn	Asn
1611	GTC	CTG	GCC	TTT	GTG	GTC	ATC	TGT	GGC	TGC	TAT	ACC	CAC	ATC	TAC	CTC	ACA	GTG	AGG	AAT
521	Val	Leu	Ala	Phe	Val	Val	Ile	Cys	Gly	Cys	Tyr	Thr	His	Ile	Tyr	Leu	Thr	Val	Arg	Asn
1671	CCT	ACC	ATT	GTG	TCC	TCA	TCA	AGC	GAC	ACC	AAG	ATT	GCC	AAG	CGC	ATG	GCC	ACA	CTC	ATC
541	Pro	Thr	Ile	Val	Ser	Ser	Ser	Ser	Asp	Thr	Lys	Ile	Ala	Lys	Arg	Met	Ala	Thr	Leu	Ile
1731	TTC	ACA	GAC	TTT	CTC	TGC	ATG	GCC	CCC	ATT	TCA	TTC	TTT	GCC	ATT	TCT	GCC	TCC	CTC	AAG
561	Phe	Thr	Asp	Phe	Leu	Cys	Met	Ala	Pro	Ile	Ser	Phe	Phe	Ala	Ile	Ser	Ala	Ser	Leu	Lys
1791	GTG	CCG	CTC	ATC	ACT	GTG	TCC	AAG	GCC	AAG	ATT	CTC	CTA	GTT	CTG	TTC	TAC	CCC	ATC	AAT
581	Val	Pro	Leu	Ile	Thr	Val	Val	Ser	Lys	Ala	Lys	Ile	Leu	Leu	Val	Phe	Tyr	Pro	Ile	Asn
1851	TCT	TGT	GCC	AAT	CCT	TTC	CTC	TAC	GCC	ATT	TTC	ACC	AAG	AAC	TTC	CGC	AGG	GAC	TTC	TTC
601	Ser	Cys	Ala	Asn	Pro	Phe	Leu	Tyr	Ala	Ile	Phe	Thr	Lys	Asn	Phe	Arg	Arg	Asp	Phe	Phe
1911	ATC	CTG	CTG	AGC	AAG	TTT	GGC	TGT	TAT	GAA	ATG	CAA	GCC	CAG	ATT	TAC	AGG	ACA	GAA	ACC
621	Ile	Leu	Leu	Ser	Lys	Phe	Gly	Cys	Tyr	Glu	Met	Gln	Ala	Gln	Ile	Tyr	Arg	Thr	Glu	Thr
1971	TCA	TCC	GCT	ACC	CAC	AAC	TTC	CAT	GCC	CGA	AAG	AGC	CAC	TGC	TCC	TCA	GCT	CCC	AGA	GTC
641	Ser	Ser	Ala	Thr	His	Asn	Phe	His	Ala	Arg	Lys	Ser	His	Cys	Ser	Ser	Ala	Pro	Arg	Val
2031	ACC	AAT	AGT	TAC	GTG	CTT	GTC	CCT	CTT	AAT	CAT	TCA	TCC	CAG	AAC	TAAAATCAA	TGTGAAAA			
661	Thr	Asn	Ser	Tyr	Val	Leu	Val	Pro	Leu	Asn	His	Ser	Ser	Gln	Asn					
2094	TG	GATCCTCACC	TTGAAGACA	ATTATGACTC	CTTCTGAAGA	GCAGGCCATG	GACTAATGG	CAATCCTACT												
2166	GCACATCTCA	TCTAATTAA	TCTCTCTGGG	TCTCTGCATG	GCAGACTGAT	CAGGGACCAT	TAATCACCCC													
2236	TTTGGCTCCT	CTCACACTTA	AATAATGGTA	ACAGCAATA	ANACAAGCA	AAACCCACA														

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Fig.7.

A)



B)

1 RELSGSR PE.P D APDGA R PGPRAGLAR..... SLTYLFVK
 1 CHHWLCHCSNRVFL.CQDSKVTEIPTDLPRNAIELRFVLTQRL

41 SQA R LNEVV S S R NA D LN S LL QNTK
 43 VIPKGSFAGFGDLEKIEISQNDVLEIVIEADVFSNLPKLHEIRIEKANNLL

91 E G T R K S C RT D T S SEFNFI E C LH T
 91 YINPEAFQNLPSRLRYLLISNTGIKHLPAVHKIQSLQ.KVLLDIQDNINIH

141 TIPG A Q MN T K YG F VQSH T IS E KE IY K
 142 IVARN SFMGLSFESVILWLSKNGIEEIH NCAFNGTQDELNLS DNN NLEE

191 MHSGA T S S LQA S SIQT I L S S T SK
 192 LPNDVFQ GAGSGPVILDISRTKVHSLPNHGLENLKKLRARSTYRLKKLPNL

241 E TS LV T R PKKE.....QNFSFSIFENFSKQC
 242 DKFVTLM EASLTYP SHCCAFANLKRQISELHPICNKSILRQIDDMTQIG

283 EST RKA N TL SAIFEENELSGWDY GF S.PKT LQ A E
 292 DQRVSIIDDEPSYG...KGSDDMYNEFDYDLCEVVLVTCSPKPDAFNPC

332 AF LN F L F L R S
 339 EDIMGYNILRVLIWFISILAITGNTTVLVVLTTSQYKLTVPREFLMCNLAF

382 F M L SQ G Y H S G
 389 ADLCIGIYLLLIASVDIHTKSQYHNYAIDWQTGAGCDAAGFFTVFASELS

432 V Y V DQ LR IPI LG L STLI TM LV
 439 VYTLTAITIERWHTITHAMQLECKVQLRHAASVMVLGWTFAFAAALFPIF

482 N VE T V ILSI I V A IR FA
 489 GISSYMKVSICLPMDIDSPLSQLYVMALLVNLVLAFFVICGCTHIYLTV

532 Q ELTAPNK K I T AF TN
 539 RNPTIVSSSDTKIAKRMATLIFTDFLCMAPI SFFAISASIKVPLITVSK

582 S V A Q LL R CKRR EL
 589 AKILLVLFYFINS CANPFLYAIFTKNERRDFFILLSKFGCYEMQAQIYRT

631 EF.. YTSNCKNGFP GASKP ATCLKLSTVHCQOPI
 639 ETSSATHNFHARKSHCSSAPRV TNSYVLVPLNHSSQN.....

693 PPRALTH rat LH/CG receptor
 639 rat FSH receptor

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Fig.8.

	(1- 19)	C	H	H	W	L	C	H	C	S	N	R	V	F	L	C	Q	-	-	D	S	K									
1	(20- 40)	V	T	E	I	P	T	D	L	P	R	N	A	I	E	L	R	F	V	-	L	T	K								
2	(41- 66)	L	R	V	I	P	K	G	S	F	A	G	F	G	D	L	E	K	I	E	I	S	Q	N	D	V					
3	(67- 90)	L	E	V	I	E	A	D	V	F	S	N	L	P	K	L	H	E	I	R	I	E	K	A	N	N					
4	(91-114)	L	L	Y	I	N	P	E	A	F	Q	N	L	P	S	L	R	Y	L	L	I	S	-	N	T	G					
5	(115-139)	I	K	H	L	P	A	V	H	K	I	Q	S	L	Q	K	V	L	L	D	I	Q	D	N	I	N					
6	(140-164)	I	H	I	V	A	R	N	S	F	M	G	L	S	F	E	S	V	I	L	W	L	S	K	N	G					
7	(165-188)	I	E	E	I	H	N	C	A	F	G	T	Q	L	D	E	L	-	L	S	D	N	N	N	N						
8	(189-212)	L	E	E	L	P	N	D	V	F	Q	G	A	S	G	P	V	I	L	D	I	S	R	T	K						
9	(213-234)	V	H	S	L	P	N	H	G	L	E	N	L	K	K	L	R	A	R	S	T	Y	R								
10	(235-251)	L	K	K	L	P	N	L	D	K	F	V	T	L	M	E	A	S													
11	(252-283)	L	T	Y	P	S	H	C	A	F	A	N	L	K	R	Q	I	S	E	L	H	P	I	C	K	S	I	L	R	Q	D
12	(284-297)	I	D	D	M	T	Q	I	G	D	Q	R	V	S	L																
13	(298-325)	I	D	D	E	P	S	Y	G	K	G	S	D	M	M	Y	N	E	F	D	Y	D	L	C	N	E	V	V	D		
14	(326-348)	V	T	C	S	P	K	P	D	A	F	N	P	C	E	D	I	M	G	Y	N	I	L	R							

Fig.9.

